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09/857,557
BB1297USPCT
PRELIMINARY AMENDMENT AND RESPONSE TO NOTIFICATION OF DEFECTIVE
RESPONSE
STATEMENT UNDER 37 1.821(g) AND 1.825(b)
SEQUENCE LISTING - CRF
SEQUENCE LISTING - 23 PAGES
COPY OF NOTIFICATION OF DEFECTIVE RESPONSE AND RAW SEQUENCE LISTING
ERROR REPORT
RETURN RECEIPT CARD



UNITED STATES PATENT AND TRADEMARK OFFICE



Rec'd PCPTO 22 MAR 2002 Page 1 of 2 #6

1 month

Commissioner for Patents, Box 501
United States Patent and Trademark Office
Washington, D.C. 20231
www.uspto.gov

U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
09/857,557	Rebecca Cahoon	BB-1297

Kening Li
E. I. Du Pont De Nemours And Company
1007 Market Street
Wilmington, DE 19898

Date Mailed: 02/20/2002

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INTERNATIONAL APPLICATION NO.

PCT/US99/28616

I.A. FILING DATE	PRIORITY DATE
12/03/1999	12/04/1998

CONFIRMATION NO. 5031
371 FORMALITIES LETTER

OC000000007485941

NOTIFICATION OF DEFECTIVE RESPONSE

The following items have been submitted by the applicant or the IB to the United States Patent and Trademark Office as an Elected Office (37 CFR 1.495):

- U.S. Basic National Fee
- Priority Document
- Biochemical Sequence Diskette
- Biochemical Sequence Listing
- Copy of IPE Report
- Copy of references cited in ISR
- Copy of the International Application
- Copy of the International Search Report
- Information Disclosure Statements
- Oath or Declaration
- Preliminary Amendments
- Request for Immediate Examination

DOCKETED
CR

FEB 28 2002

The following items **MUST** be furnished within the period set forth below in order to complete the requirements for acceptance under 35 U.S.C. 371:

Applicant is required to complete the response within a time limit of ONE MONTH from the date of this Notification or within the time remaining in the response set forth in the Notification of Missing Requirements, whichever is the longer. No extension of this time limit may be granted under 37 CFR 1.136, but the period for response set in the Notification of Missing Requirements may be extended under 37 CFR 1.136(a).

The following items **MUST** be furnished within the period set forth below:

- The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):
 - See attached raw sequence listing error report.

- APPLICANT MUST PROVIDE:
 - An initial or substitute paper copy or compact disc of the "Sequence Listing," as well as an amendment directing its entry into the specification.
- For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:
 - For Rules Interpretation, call (703) 308-4216
 - To Purchase PatentIn Software, call (703) 306-2600
 - For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

A copy of this notice MUST be returned with the response.

JOHN L ANDERSON

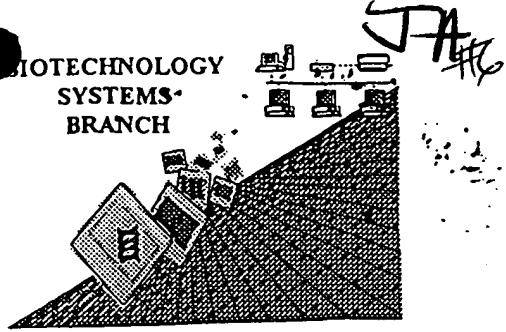
Telephone: (703) 308-9116

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
09/857,557	PCT/US99/28616	BB-1297

FORM PCT/DO/EO/916 (371 Formalities Notice)

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857557
Source: PCT09
Date Processed by STIC: 10/29/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/957557</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIA" HEADERS, WHICH WERE INSERTED BY PI		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequen <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent:	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rule:	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

3 <110> APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
5 <120> TITLE OF INVENTION: PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE
7 <130> FILE REFERENCE: BB1297
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/857,557
C--> 10 <141> CURRENT FILING DATE: 2001-09-22
12 <150> PRIOR APPLICATION NUMBER: 60/110,865
W--> 13 <151> PRIOR FILING DATE: 1998-DECEMBER-04
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 565
21 <212> TYPE: DNA
22 <213> ORGANISM: Zea mays
24 <220> FEATURE:
25 <221> NAME/KEY: unsure
26 <222> LOCATION: (5)..(9)
28 <220> FEATURE:
29 <221> NAME/KEY: unsure
30 <222> LOCATION: (450)
32 <220> FEATURE:
33 <221> NAME/KEY: unsure
34 <222> LOCATION: (549)
36 <400> SEQUENCE: 1

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38 gcctacccta ctacactcggt gccgattcgg cacgagcgcg gacggtcgccc accaccgctc 120
39 ccctccctct cccccctcgtt gcccagcggc aattaccaca gcctcccccag caagccggga 180
40 tggctgcactt caaggcatcg ttccgggtt agctcagcgc cgcttccttc ctcgactcca 240
41 gcaggggacc tctcgccatc cacaagggtt atttacgtt tcaaaggaag ggcaaacgag 300
42 ctatttactt gagaaggaca tgctgttcta tgcaacaggc tccaccacca gcatggcctg 360
43 ggccgagctgt tgctgagcctt ggccggagtc atggatggc ccaaaggccta tctcgattgt 420
W--> 44 tggttcaactt ggttccatag gaacacagan atggacattt gttgcggaga atcctgtata 480
45 gttcagagttt gttgctctt ctgtggatc caatgtcagc cttcttagtgc atcaggtcaa 540
W--> 46 aacattcana cctaagtgg ttccgg 565

48 <210> SEQ ID NO: 2
49 <211> LENGTH: 63
50 <212> TYPE: PRT
51 <213> ORGANISM: Zea mays
53 <220> FEATURE:
54 <221> NAME/KEY: UNSURE
55 <222> LOCATION: (25)
57 <220> FEATURE:
58 <221> NAME/KEY: UNSURE
59 <222> LOCATION: (58)

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

61 <400> SEQUENCE: 2
62 Ala Trp Pro Glu Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
63 1 5 10 15
W--> 65 Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

66	20	25	30
68	Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr		
69	35	40	45
W--> 71	Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg		
72	50	55	60
74	<210> SEQ ID NO: 3		
75	<211> LENGTH: 868		
76	<212> TYPE: DNA		
77	<213> ORGANISM: Zea mays		
79	<220> FEATURE:		
80	<221> NAME/KEY: unsure		
81	<222> LOCATION: (343)		
83	<220> FEATURE:		
84	<221> NAME/KEY: unsure		
85	<222> LOCATION: (356)		
87	<220> FEATURE:		
88	<221> NAME/KEY: unsure		
89	<222> LOCATION: (367)		
91	<220> FEATURE:		
92	<221> NAME/KEY: unsure		
93	<222> LOCATION: (789)		
95	<220> FEATURE:		
96	<221> NAME/KEY: unsure		
97	<222> LOCATION: (862)		
99	<400> SEQUENCE: 3		
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101	caagggtgtca tagaagggtgc tcgccatcca gatgoagtta cagttgtcac agggatagta	120	
102	ggtttgtcag ggctgaagcc tacagttgtc gcaattgaag ctggtaaaga catagcattg	180	
103	gcaaacaag agacacttat tgcaggtggt cctttgtgc ttcccccttc acacaaacac	240	
104	aaagtgaaaa ttcttccagc tgattctgag cactotgcaa tatttcagtg tatacaaggc	300	
W--> 105	ttgtccgaag gtgcacttcg tcgcattatt ctaactgcac cagtgggc tttcaanngac	360	
W--> 106	tggccannttg acaggctgaa agatgtaaaa gttgctgacg ctttaaagca tccaaactgg	420	
107	aatatggaa ggaagatcac agtagattct gctactttat tcaacaaggg tttagaagtt	480	
108	attgaagcac attattttt tggtgctgaa tatgatgaca ttgagattgt gattcaccca	540	
109	cagtttatca tacactctat gttgaaacc caggattcat ctgtccttagc tcagttggga	600	
110	tggccagata tgcggttacc aatcttatac accttacat gccagatag gagtcctgag	660	
111	cgtcgtaat gagaaggccg tggagttgtt cattgacgag aagattagct acctggacat	720	
112	attcaagggtg gtggagctt catgtaacgc gcatcggAAC agctggtaac aaccgtcact	780	
W--> 113	ggaggaatn tcattacatc gtggcaagaa tatgcagcat cacaacatct ctggctgagc	840	
W--> 114	tgtcctgcac atagtctcac anacttgt	868	or
116	<210> SEQ ID NO: 4		
117	<211> LENGTH: 217		
118	<212> TYPE: PRT		
119	<213> ORGANISM: Zea mays		
121	<220> FEATURE:		
122	<221> NAME/KEY: UNSURE		
123	<222> LOCATION: (115)		
125	<220> FEATURE:		
126	<221> NAME/KEY: UNSURE		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

127 <222> LOCATION: (119)
 129 <220> FEATURE:
 130 <221> NAME/KEY: UNSURE
 131 <222> LOCATION: (123)
 133 <400> SEQUENCE: 4
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 135 1 5 10 15
 137 Ile Pro Gly Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Asp Ala
 138 20 25 30
 140 Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
 141 35 40 45
 143 Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
 144 50 55 60
 146 Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
 147 65 70 75 80
 149 Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
 150 85 90 95
 152 Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
 153 100 105 110
 W--> 155 Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro (Xaa) Asp Arg Leu Lys Asp ✓
 156 115 120 125
 158 Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
 159 130 135 140
 161 Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
 162 145 150 155 160
 164 Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
 165 165 170 175
 167 Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
 168 180 185 190
 170 Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
 171 195 200 205
 173 Leu Tyr Thr Leu Ser Trp Pro Asp Arg
 174 210 215
 176 <210> SEQ ID NO: 5
 177 <211> LENGTH: 1901
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Oryza sativa
 181 <400> SEQUENCE: 5
 182 acactatgac catgattacg ccaagcgcgc aattaaccct cactaaaggg aacaaaagct 60
 183 ggagctccac cgccgtggcg gcccgtctag aactagtgg a tccccgggc tgcaggaatt 120
 184 cgccacgagg tttaaaccag acgtcgagtc gagcattaac tcagtcaggg tggccatggc 180
 185 gctcaaggtc gtctcttcc cccgggactt ggccgcggtc tcattcctcg actccaacag 240
 186 aggaggagct ttcaaccagc tcaaagtgg a cttcccg ttt caaacgaggg acagaagagc 300
 187 agttccctg agaaggactt gctgttcaat gcaacaggtt ccaccaccag catggcctgg 360
 188 tcgagccgtt gttgaacctg ggaggaggtc atggatggc cccaa gccta tctcaattgt 420
 189 tggctcaacc ggttctattg gcacacagac attggacata gttgcggaga atccagataa 480
 190 attccgggtt gttgcttgc ctgctggctc caatgtgact cttctagctg atcaggtgaa 540
 191 aacattcaaa ccaaagctt ttgctgtaa aatgagtca tttagttgatg agctaaagga 600
 192 agccttagct gattgtgatt ggaagccaga aattattccct ggtgagcaag gtgtcataga 660

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
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Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

193 gtttgctcg caccagatg cagttacagt tgttactggg atagtaggt gtgcaggact 720
 194 gaaggctaca gttgctgcaa ttgaagctgg gaaagatata gcattggcga acaaagagac 780
 195 acttatttgc ggtggcctt ttgtgcttcc cttgcacaa aagcacaaag taaaatact 840
 196 tcctgctgat tctgagca ctgctatatt tcagtgtata caaggcttc ccgaaggagc 900
 197 acttcggccgc attattttga ctgcattcagg tgggtcttc agggactggc cagttgacaa 960
 198 gttgaaagaa gtaaaagttt ctgatgctt aaagcaccgg aactggaata tggggaaagaa 1020
 199 gattactgtt gattctgcta cattattcaa caagggtta gaagttattt aagcacatta 1080
 200 tttatattttgtt gctgaatacg atgacattga aatttgttgc caccacaaat ctatcataca 1140
 201 ctctatgatt gaaaccagg attcatctgt gttgctcaa ctggatggc cagatatgcg 1200
 202 gataccaacc ttatacacca tgtcttggcc agacagaatc tattgtctcg aggtcacctg 1260
 203 gccccgacta gatcttgca agctgggttc actgacattc aaagctcctg acaatgtgaa 1320
 204 ataccctcg atggatctcg cctatgcagc tggaaagagct gggggcacca tgacaggagt 1380
 205 tctgagtgtc gctaattgaga aggctgttga gttgttcatc gatgaaaaga tcgggtacct 1440
 206 ggacatcttc aaggtgggtgg agctgacatg cgacgctcat cggaatgagc tagtaacaag 1500
 207 gccatcactg gaggagatca tacattatga tctgtggcgg agggagtatg ctgccagcct 1560
 208 acagccatcc actggcctca gcccgttacc tgtctagtac ttgttagcaat aaaaaattac 1620
 209 agtagcattt tacactactg ccgtgccagc tccatgcata gtcagcagct ggccactctc 1680
 210 tagctatatac tagatgcgag agaattttaa ggtatgtaat catgccttca catgaataaa 1740
 211 tcgttcgtcc gtgcgttgc tattcatgtt aattttgacg gatggtcaag taaaataaac 1800
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 213 aattcccccct atagttagtc gtattacgcg cgctcactgg c 1901
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 216 <211> LENGTH: 473
 217 <212> TYPE: PRT
 218 <213> ORGANISM: Oryza sativa
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 224 Phe Leu Asp Ser Asn Arg Gly Gly Ala Phe Asn Gln Leu Lys Val Asp
 225 20 25 30
 227 Leu Pro Phe Gln Thr Arg Asp Arg Arg Ala Val Ser Leu Arg Arg Thr
 228 35 40 45
 230 Cys Cys Ser Met Gln Gln Ala Pro Pro Pro Ala Trp Pro Gly Arg Ala
 231 50 55 60
 233 Val Val Glu Pro Gly Arg Arg Ser Trp Asp Gly Pro Lys Pro Ile Ser
 234 65 70 75 80
 236 Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu Asp Ile Val
 237 85 90 95
 239 Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser
 240 100 105 110
 242 Asn Val Thr Leu Leu Ala Asp Gln Val Lys Thr Phe Lys Pro Lys Leu
 243 115 120 125
 245 Val Ala Val Arg Asn Glu Ser Leu Val Asp Glu Leu Lys Glu Ala Leu
 246 130 135 140
 248 Ala Asp Cys Asp Trp Lys Pro Glu Ile Ile Pro Gly Glu Gln Gly Val
 249 145 150 155 160
 251 Ile Glu Val Ala Arg His Pro Asp Ala Val Thr Val Val Thr Gly Ile
 252 165 170 175
 254 Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile Glu Ala Gly

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
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Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

255	180	185	190
257	Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro		
258	195	200	205
260	Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala		
261	210	215	220
263	Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu		
264	225	230	235
266	Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg		
267	245	250	255
269	Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu		
270	260	265	270
272	Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala		
273	275	280	285
275	Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe		
276	290	295	300
278	Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile		
279	305	310	315
281	Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu		
282	325	330	335
284	Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro		
285	340	345	350
287	Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys		
288	355	360	365
290	Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro		
291	370	375	380
293	Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr		
294	385	390	395
296	Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp		
297	405	410	415
299	Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys		
300	420	425	430
302	Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile		
303	435	440	445
305	Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro		
306	450	455	460
308	Ser Thr Gly Leu Ser Pro Val Pro Val		
309	465	470	
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312	<211> LENGTH: 1592		
313	<212> TYPE: DNA		
314	<213> ORGANISM: Glycine max		
316	<220> FEATURE:		
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321	<221> NAME/KEY: unsure		
322	<222> LOCATION: (1402)		
324	<400> SEQUENCE: 7		
325	gctgggttcaa ctgaggtgat ggctttcaat ttgccttc tc ccggccaa gt gaaggccctta	60	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
TIME: 13:15:17

Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:37 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:71 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:114 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:155 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:348 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:451 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:531 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:532 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:533 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:553 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:583 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:650 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:651 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,557

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Input Set : A:\BB1297 PCT Seq List.txt
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L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:652 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:708 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:709 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:730 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:749 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15